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About: Results were produced by the GenCore software, version 4.5,
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Date: May 2, 2000 4:41 AM

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; Patent No. 5614609
; GENERAL INFORMATION:
; APPLICANT: Ib ez, Carlos F.
; APPLICANT: Ryd n, Mikael
; APPLICANT: J invall, Henrik
; TITLE OF INVENTION: A No. 5614609e1 Serine Threonine Kinase Receptor
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/341,916
; FILING DATE: Herewith
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 1459.0230001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1482 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
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US-08-341-916-1

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1051 ATCATGAACACTATAGATATACCCCCAGAATCCTAAAGTGGGAACCAAGAG    1100

367 gTyrMetAlaProGluMetLeuAspAspThrMetAsnValAsnIlePheG    384
1101 GTATATGGCTCCCGAAATGCTTGATGAACAAATGAACGTCAACATCTTTG    1150

384 luSerPheLysArgAlaAspIleTyrSerValGlyLeuValTyrTrpGlu    400
1151 AGTCCTTCAAGCGAGCTGACATTTATTCGGTGGGGCTTGTTTACTGGGAA    1200

401 IleAlaArgArgCysSerValGlyGlyIleValGluGluTyrGlnLeuPr    417
1201 ATAGCCTCGAAGGTGTCAGTTGGAGGAACTGTTGAAGAGTACCAGTTGCC    1250

417 oTyrTyrAspMetValProSerAspProSerIleGluGluMetArgLysV    434
1251 TTATTATGACATGGTGCCTTCAGATCCTTCCATAGAGGAAATGAGGAAGG    1300

434 alValCysAspGlnLysLysPheArgProSerIleProAsnGlnTrpGlnSer    450
1301 TCGTTTGTGATCAGAAACTCCGACAAAAATCTCCCAAACCAGTGGCAAAGC    1350

451 CysGluAlaLeuArgValMetGlyArgIleMetArgGluCysTrpTyrAl    467
1351 TGTGAGGCGCTCCGGGTCATGGGAAGAATAATGCGGGAGTGCTGGTATGC    1400

467 aAsnGlyAlaAlaArgLeuThrAlaLeuArgIleLysLysThrIleSerG    484
1401 CAACGGGGCAGCTCGCCTGACACCGCCCTGCGAAGAAGACCATTTCTC    1450

484 lnLeuCysValLysSerGlnAspCysLysSerAla    493
1451 AGTTGTGTGTCAAGGAAGACTGTAAGGCC    1479
```

GENERAL INFORMATION:
    APPLICANT: Ib ez, Carlos F.
    APPLICANT: Ryd n, Mikael
    APPLICANT: J rnvall, Henrik
    TITLE OF INVENTION: A No. 581124s e1 Serine Threonine Kinase Receptor
    NUMBER OF SEQUENCES: 6
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Sterne, Kessler, Goldstein & Fox
    STREET: 1100 New York Avenue, Suite 600
    CITY: Washington
    STATE: DC
    COUNTRY: USA
    ZIP: 20005
    COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/805,169
    FILING DATE: 24-FEB-1997
    CLASSIFICATION: 536
    PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/341,916
    FILING DATE: 15-NOV-1994
    ATTORNEY/AGENT INFORMATION:
    NAME: Goldstein, Jorge A.
    REGISTRATION NUMBER: 29,021
    REFERENCE/DOCKET NUMBER: 1459.0230001
    TELECOMMUNICATION INFORMATION:
    TELEPHONE: (202)371-2600
    TELEFAX: (202)371-2540
    INFORMATION FOR SEQ ID NO: 1:
    SEQUENCE CHARACTERISTICS:
    LENGTH: 1482 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: both
    TOPOLOGY: both
    FEATURE:
    NAME/KEY: CDS
    LOCATION: 1..1482

US-08-805-169-1

alignment_scores:
    Quality: 2449.00   Length: 493
    Ratio: 5.091   Gaps: 0
Percent Similarity: 97.566   Percent Identity: 93.103

alignment_block:
US 069-228-2 x US-08-805-169-1
Align seg 1/1 to: US-08-805-169-1

Align seg 1/1 to: from: 1 to: 1482

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  1 MetThrArgAlaLeuCysSerAlaLeuArgGlnAlaLeuLeuLeuLeuAl  17
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  1 ATGACCCGAGCAAGCCGCCTCCGCACTGAGCCGTGCGCCTCCTGGTGGC  50

 17 aAlaAlaAlaGluLeuSerProGlyLeuCysScValCysLeuLeuCysA  34
    ||||::::::::||:::::
 51 ACTGGCCTCCGACCTTGGGCGCCAGGAACTGAAGTGTGTCGTCTTTTGTGTG  100

 34 spSerSerAsnPheThrCysGlnThrGluGlyAlaCysTrpAlaSerVal  50
    ||||||||||||||||||||||||||
101 ATTCCTCAAACTTTACCTCCCAAACCGAGGAGCATGCTGGGCCTCTGTC  150

 51 MetLeuThrAsnGlyLysGlnValIleIleLysSerCysValSerLeuPr  67
    ||||||||||||||||||||||||||||||
151 ATGCTAACCAACGGGAAAGAACAGGTGATCAAAATCGTGCGTGCCCTCCC  200

 67 oGluLeuAsnAlaGlnValPheCysHisSerSerAsnAsnValThrLysT  84
    ||||||||||||||||||||||||||||||||||||||
201 GGAACTAAATGCTCAGGTCTTCTGTCACAGTTCCAACAACGTGACCAAGA  250
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INFORMATION FOR SEQ ID NO: 1:

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 84 hrGluCysCysPheThrAspPheCysAsnAsnIleThrLeuHisLeuPro  100
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251 CCGAAATGTTGCTTCACAGACTTCTGCAACAACATCACTCTGCACCTTCCC  300

101 ThrAlaSerProAsnAlaProLysLysGlyProMetGluLeuAlaIeIl  117
    ||||||||||||||||||::::|||
301 ACAGCATCTCCAGATCCCCCAGACTTGGCCCCCACAGAGGCTGACAGTTGT  350

117 eIeIeThrValProValCysLeuLeuSerIleAlaAlaLaMetLeuThrValT  134
    |||||||||||||||||||||||||||::|
351 TATCACTGTACCTGTTTGCCTCCTCCGTCCATCGCAGCCATGCTAACGATAT  400

134 rpAlaCysGlnGlyArgGlnCysSerTyrArgGlyLysLysArgProAsn  150
    ||||||  ||||::||||||||||||||||||
401 GGGCCTGCCAGGACCCCAGTGCACATACAGGGAAGAAGAGACACAAT  450

151 ValGluGluProLeuSerGluCysAsnLeuValAsnAlaGlyLysThrIe  167
    |||||||||||||::::|||||||||||
451 GTGGAGGAACCACTGGCAGAATACAGCCTTGTCAATGCTGGAAAAACCCT  500

167 uLysAspLeuIleTyrAspValThrAlaSerGlySerGlySerGlyLeuP  184
    ||||||:|:|||||||::||||||||||||
501 CAAAGACTCGATTTATGATGTCACACTGGGTCAGGATCTGGCCTGC  550

184 roLeuLeuValGlnArgThrIleAlaArgThrIleValLeuGlnGluIle  200
    |||||||||||||||||||||||||||||||
551 CTCTTTGGTTCAAAGAACCAATCCGAAGAACAGAATTGTACTTCAGAAAIC  600

201 ValGlyLysGlyArgPheGlyGluValTrpHisGlyArgTrpCysGlyGl  217
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601 GTAGGAAAAGGTCGGTTTGGGGAAGTGTGGCACGGAAGATGGTGTGGAGA  650

217 uAspValAlaValLysIlePheSerSerArgAspGluArgSerTrpPheA  234
    |||||||||||||||||||||||||||||||
651 AGATGTGGCTGTGAAAATATTCTCCTCCAGAGATGAGAGAcTCTGGTTCC  700

234 rgGluLeuGluIleTyrGlnThrValMetLeuArgHisGluAsnIleLeu  250
    |||||||||||||||||||||||||||||||
701 GTGAGGCAGAAATTTATCAGACGGTAAATGCTGAGACAICAGAGAATTCTC  750

251 GlyPheIleAlaAlaAspAsnLysAspAsnGlyThrTrpThrGlnLeuTr  267
    ||||||||||||||||||||||||||||||
751 GGTTTCATCGCGGCCGACAACAAAGATAATGGAACCTGGACTCAGCTTTG  800

267 pLeuValSerGluTyrHisGluGlnGlySerLeuTyrAspTyrLeuAsnA  284
    ||||||||||||||||||||||||||||
801 GCTTGTGTCAGAGTACCACGACCAGGGCTCCTTATATGACTATTTGAATA  850

284 rgAsnIleValThrValAlaGlyMetIleLysLeuAlaLeuSerIeAla  300
    |||||||||||||||||::::|||
851 GAAACATAGTGACCGTGGCTGGAATGGTCAAGTTGGCGCTTTCAATTAGCG  900

301 SerGlyLeuAlaHisLeuHisMetGluIleValGlyThrGlnGlyLysPr  317
    ||||||||||||||||||||||||||||||
901 AGTGGTCTGGCTCACCTACACATGGAGATCGTGGGCACTCAAGGTAAGCC  950

317 oAlaIleAlaHisArgAspLeuLysSerLysAsnIleLeuValLysLysC  334
    ||||||||||||||  ||||||||||||||
951 TGCTATTGCTCACCGAGATATAAAGTCAAAGAATATCTTAGTCAAAAAGT  1000

334 ysGluThrCysAlaIleAlaAspLeuGlyLeuAlaValLysHisAspSer  350
    |::::|||||||||||||||||||||||||||||||
1001 GTGACACTTGTGCCAТAGCTGACTTAGGCGTGGCTGTGAAACATGATTCT  1050

351 IleLeuAsnThrIleAspIeProGlnAsnProLysValGlyThrLysAr  367
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1051 ATCATGAACACTATAGATATACCCCAGAATCCTAAAGTGGGAACCAAGAG  1100

367 gTyrMetAlaProGluMetLeuAspAspThrMetAsnValAsnIlePheG  384
    |||||||||||||||||||||||||||||
1101 GTATATGGCTCCCGAAATGCTTGATGATACAATGAACGTCAACAtCTTTG  1150
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